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*      20      *      40      *      60      *      80      *      100
TXE   : -----MNQPPPSALETCLVTDIKRARTFYEITFCYSVAADDRF-CAEAGERCVLLFLHGSDPHGSVMPFGTIPPHDGSG : 79
Tfla  : -----MTSKLTLTAELDRMLAFYTNMGAQHHEQADA-FTIQLGVSQVQFR--A-----AADGTKP : 57
3GHJ_A : XGSSHHHHHSSGRENLVYFQGVVXNIKGLFVAVRVKNDKSSCFYTEILGFEAGLLDSARRWNSLWVSGRAGVVVLQ-----EKENWQ : 85
NE_635587. : -----LETGVVAIDRACAFYACVILGLQVHRDARM-AAVAIAPACVLLFLQGSTTTTVRLPGGTIPPHDGHG : 70
EDY82674.1 : -----MKAKRIFETILVAEOLPAAKLFYRDTGLELLRESE-IVIVRLQDS-VLIV----FDPRKSSPPGRAVPSHGTSG : 70
YE_446160. : -----MPTPPRLALETSLVADLIAAAECFYGDVILGLDVLRTEGNHITRCGPG-VVHV----FDPAASR-DRTSLPAHGAEG : 72

0      *      120      *      140      *      160      *      180      *      200
TXE   : FVHIGFGTSSSELP---AQRTRLAEYGVATE-STITWP-RGGTSTYFRDEDGHLLEIVTPGIWKIY----- : 140
Tfla  : FYHIAINIAANHFQEGKALSGFGELLTENDEDDQAYPFFNAYSQVVEDESNITELISRQCAAEVLDKPFSAQQLLSIGEI-NITTSDEVEQAATRLKQ : 155
3GHJ_A : QQHFSEFVKESETE---PLKKALESKGVSH-GEVNQEWXQAVSLYFADENCHALFETAL----- : 141
NE_635587. : HTNYALAIATESIA---AWEAHLHACVAIE-GRTQWP-GGGQSMYFRDEDDHIVLALATPGLWPNY----- : 131
EDY82674.1 : EGHIAFAATDEETR---EWFVHLESKGVETE-SVVEWG-EGGESLYVRDEAGNSVVFAPSTLWGGGWD---FAK----- : 136
YE_446160. : FVHVAFGVPTDQIA---ARRRHFNRRHVAIE-DTTQVGDGQRSLYVRDEAGNSVLEIVSSTLWSTTAR---AERLRFVRFVLDLDTAES-RFEVQFCN : 161

00      *      220      *      240      *      260      *      280      *
TXE   : ----- : -
Tfla  : AELFVKLDQIEPAGLNFIGDQDLFLLGPPGRRWLFSEFVAVIYPLQMELDNGVSLAITETGEIVI----- : 221
3GHJ_A : ----- : -
NE_635587. : ----- : -
EDY82674.1 : ----- : -
YE_446160. : ETLRPILKLLNPTILRLVAERLA----RYGVGFAAMDVFVDQ-----RDRLRNLMKEDGRLKRTLLGMVVGHLTQDELDAYLAHKDEVRRRTVPMIL : 247

300      *
TXE   : ----- : -
Tfla  : ----- : -
3GHJ_A : ----- : -
NE_635587. : ----- : -
EDY82674.1 : ----- : -
YE_446160. : LARAQDQIDDIVERVRTQAEGA : 269

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**S3 Fig.** Sequence alignment of TxeA, TflA, and VOC superfamily proteins. The amino acid sequence of VOC superfamily proteins and the corresponding GenBank accession numbers are as follows: 3GHJ\_A; Chain A, Crystal Structure From The metagenomic protein from Halifax harbour sewage outfall, NP\_635587; lactoyl glutathione lyase from *Xanthomonas campestris* pv.; glyoxalase family protein from *Verrucomicrobiae bacterium* DG1235, YP\_446160; glyoxalase family protein from *Salinibacterruber* DSM 13855. The highlighted red letters indicate the conserved amino acids in metal-binding motif.